



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/811,138

DATE: 09/14/2004

TIME: 10:27:35

Input Set : A:\US Utility 050229-0421 Sequence Listing.txt

Output Set: N:\CRF4\09142004\J811138.raw

3 <110> APPLICANT: University of Kentucky Research Foundation
 4 Daunert, Sylvia
 5 Rowe, Laura
 6 Dikici, Emre
 7 Deo, Sapna Kamalakar
 9 <120> TITLE OF INVENTION: AEQUORIN AND OBELIN MUTANTS WITH DIFFERING WAVELENGTHS AND
 10 BIOLUMINESCENCE
 12 <130> FILE REFERENCE: 050229-0421
 14 <140> CURRENT APPLICATION NUMBER: 10/811,138
 15 <141> CURRENT FILING DATE: 2004-03-29
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn version 3.2
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 861
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Aequorea victoria
 26 <400> SEQUENCE: 1

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29	tctcgacaac aacaagcaaa catgacaagc aaacaatact	cagtcaagct tacatcagac	120
31	ttcgacaacc caagatggat tggacgacac aagcatatgt	tcaatttcct tgatgtcaac	180
33	cacaatggaa aaatctctct tgacgagatg gtctacaagg	catctgatat tgtcatcaat	240
35	aaccttggag caacacctga gcaagccaaa cgacacaaag	atgctgtaga agccttcttc	300
37	ggaggagctg gaatgaaata tgggtgtggaa actgattggc	ctgcatatat tgaaggatgg	360
39	aaaaaattgg ctactgatga attggagaaa tacgccaaaa	acgaaccaac gtcacatccg	420
41	atatgggggtg atgctttgtt tgatategtt gacaaagatc	aaaatggagc cattacactg	480
43	gatgaatgga aagcatcacac caaagctgct ggtatcatcc	aatcatcaga agattgagag	540
45	gaaacattca gagtgtgcga tattgatgaa agtggacaac	tcgatgttga tgagatgaca	600
47	agacaacatt taggattttg gtacaccatg gatcctgctt	gcgaaaagct ctacggtgga	660
49	gctgtccctt aagaagctct acggtgggtga tgcaccctgg	gaagatgatg tgattttgaa	720
51	taaaacactg atgaattcaa tcaaaatttt ccaaattttt	gaacgatttc aatcgtttgt	780
53	gttgattttt gtaattagga acagattaaa tcgaatgatt	agttgttttt ttaatcaaca	840
55	gaacttacia atcgaaaaag t		861

58 <210> SEQ ID NO: 2
 59 <211> LENGTH: 189
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Aequorea victoria
 63 <400> SEQUENCE: 2

65	Val Lys Leu Thr Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His	
66	1 5 10 15	
69	Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser	
70	20 25 30	
73	Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	
74	35 40 45	



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77 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
78      50                      55                      60
81 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro
82 65                      70                      75                      80
85 Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys
86                      85                      90                      95
89 Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
90                      100                      105                      110
93 Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu
94                      115                      120                      125
97 Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp
98      130                      135                      140
101 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
102 145                      150                      155                      160
105 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
106                      165                      170                      175
109 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
110      180                      185
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 861
115 <212> TYPE: DNA
116 <213> ORGANISM: Aequorea victoria
118 <400> SEQUENCE: 3
119 aatgcaattc atctttgcat caaagaatta catcaaactc ctagttgata aactaaattg      60
121 tctcgacaac aacaagcaaa catgacaagc aaacaatact cagtcaagct tacatcagac      120
123 ttcgacaacc caagatggat tggacgacac aagcatatgt tcaatttcct tgatgtcaac      180
125 cacaatggaa aaatctctct tgacgagatg gtctacaagg catctgatat tgatcatcaat      240
127 aaccttggag caacacctga gcaagccaaa cgacacaaaag atgctgtaga agccttcttc      300
129 ggaggagctg gaatgaaata tgggtgtggaa actgattggc ctgcatatat tgaaggatgg      360
131 aaaaaattgg ctactgatga attggagaaa tacgccaaaa acgaaccaac gctcatccgt      420
133 atatgggggtg atgctttgtt tgatatcgtt gacaaagatc aaaatggagc cattacactg      480
135 gatgaatgga aagcatcacac caaagctgct ggtatcatcc aatcatcaga agatagcgag      540
137 gaaacattca gagtgagcga tattgatgaa agtggacaac tcgatgttga tgagatgaca      600
139 agacaacatt taggattttg gtacaccatg gatcctgcta gcgaaaagct ctacggtgga      660
141 gctgtccctt aagaagctct acggtggtga tgcaccctgg gaagatgatg tgattttgaa      720
143 taaaacactg atgaattcaa tcaaaatttt ccaaattttt gaacgatttc aatcgtttgt      780
145 gttgattttt gtaattagga acagattaaa tcgaatgatt agttgttttt ttaatcaaca      840
147 gaacttacia atcgaaaaag t
150 <210> SEQ ID NO: 4
151 <211> LENGTH: 189
152 <212> TYPE: PRT
153 <213> ORGANISM: Aequorea victoria
155 <400> SEQUENCE: 4
157 Val Lys Leu Thr Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His
158 1                      5                      10                      15
161 Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser
162      20                      25                      30
165 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
166      35                      40                      45

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169 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
170      50                      55                      60
173 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro
174 65                      70                      75                      80
177 Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys
178                      85                      90                      95
181 Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
182                      100                     105                     110
185 Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu
186                      115                     120                     125
189 Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp
190                      130                     135                     140
193 Ser Glu Glu Thr Phe Arg Val Ser Asp Ile Asp Glu Ser Gly Gln Leu
194 145                     150                     155                     160
197 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
198                      165                     170                     175
201 Asp Pro Ala Ser Glu Lys Leu Tyr Gly Gly Ala Val Pro
202                      180                     185
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 662
207 <212> TYPE: DNA
208 <213> ORGANISM: Obelia longissima
210 <400> SEQUENCE: 5
211 acgatcgaac caaacaactc agctcacagc tactgaacaa ctcttggtgt gtacaatcaa      60
213 aatgtcttca aaatacgcag ttaaaactcaa gactgacttt gataatccac gatggatcaa      120
215 aagacacaag cacatgtttg atttcctcga catcaatgga aatggaaaaa tcaccctcga      180
217 tgaaattgtg tocaaggcat ctgatgacat atgtgccaaag ctogaagcca caccagaaca      240
219 aacaaaacgc catcaagttt gtgttggaagc tttctttaga ggatgtggaa tggaatatgg      300
221 taaagaaatt gccttcccac aattcctcga tggatggaaa caattggcga cttcagaact      360
223 caagaaatgg gcaagaaacg aacctactct cattcgtgaa tggggagatg ctgtctttga      420
225 tattttcgac aaagatggaa gtggtacaat cactttggac gaatggaaaag cttatggaaa      480
227 aatctctggt atctctccat cacaagaaga ttgtgaagcg acatttcgac attgcgattt      540
229 ggacaacagt ggtgaccttg atgttgacga gatgacaaga caacatcttg gattctggta      600
231 cactttggac ccagaagctg atggtctcta tggcaacgga gttccctaag ctttttttcg      660
233 aa
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 195
238 <212> TYPE: PRT
239 <213> ORGANISM: Obelia longissima
241 <400> SEQUENCE: 6
243 Met Ser Ser Lys Tyr Ala Val Lys Leu Lys Thr Asp Phe Asp Asn Pro
244 1                      5                      10                      15
247 Arg Trp Ile Lys Arg His Lys His Met Phe Asp Phe Leu Asp Ile Asn
248                      20                      25                      30
251 Gly Asn Gly Lys Ile Thr Leu Asp Glu Ile Val Ser Lys Ala Ser Asp
252                      35                      40                      45
255 Asp Ile Cys Ala Lys Leu Glu Ala Thr Pro Glu Gln Thr Lys Arg His
256                      50                      55                      60
259 Gln Val Cys Val Glu Ala Phe Phe Arg Gly Cys Gly Met Glu Tyr Gly

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```

260 65              70              75              80
263 Lys Glu Ile Ala Phe Pro Gln Phe Leu Asp Gly Trp Lys Gln Leu Ala
264              85              90              95
267 Thr Ser Glu Leu Lys Lys Trp Ala Arg Asn Glu Pro Thr Leu Ile Arg
268              100             105             110
271 Glu Trp Gly Asp Ala Val Phe Asp Ile Phe Asp Lys Asp Gly Ser Gly
272              115             120             125
275 Thr Ile Thr Leu Asp Glu Trp Lys Ala Tyr Gly Lys Ile Ser Gly Ile
276              130             135             140
279 Ser Pro Ser Gln Glu Asp Cys Glu Ala Thr Phe Arg His Cys Asp Leu
280 145             150             155             160
283 Asp Asn Ser Gly Asp Leu Asp Val Asp Glu Met Thr Arg Gln His Leu
284              165             170             175
287 Gly Phe Trp Tyr Thr Leu Asp Pro Glu Ala Asp Gly Leu Tyr Gly Asn
288              180             185             190
291 Gly Val Pro
292              195

```

VERIFICATION SUMMARY

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